

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 3, 2005, 13:50:51 ; Search time 170 Seconds

(without alignments)  
45.183 Million cell updates/sec

Title: US-10-018-964-3\_copy\_1\_15

Perfect score: 87

Sequence: 1 YGSPFGARRRNCYE 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	319	1	MYOD_HUMAN
2	87	100.0	320	2	075371
3	84	96.6	150	2	077799
4	84	96.6	318	2	075882
5	84	96.6	319	1	MYOD_PIG
6	84	96.6	319	1	MYOD_SHEEP
7	84	96.6	318	1	MYOD_MOUSE
8	63	72.4	318	1	MYOD_MOUSE
9	63	72.4	318	2	08C6B1
10	60	69.0	297	2	MYOD_COTJA
11	60	69.0	297	2	06DV59
12	60	69.0	298	1	MYOD_CHICK
13	57	65.5	289	1	MYOD_XENTLA
14	57	65.5	289	2	08AVZ0
15	50	57.5	172	2	075V41
16	50	57.5	172	2	075V42
17	49.5	56.9	288	2	07T109
18	48	55.2	652	2	08MSM9
19	48	55.2	652	2	08MSX0
20	47	54.0	271	1	FRAL_HUMAN
21	47	54.0	273	1	FRAL_MOUSE
22	47	54.0	273	2	07TMD4
23	47	54.0	275	1	FRAL_RAT
24	47	54.0	652	2	08MSX1
25	47	54.0	2340	2	07RBD0
26	46	52.9	332	2	090566
27	45.5	52.3	913	2	07X936
28	45	51.7	120	2	092WY5
29	45	51.7	139	2	06ZAR3
30	45	51.7	1184	1	DP3A_MYCBO
31	45	51.7	1184	1	DP3A_MYCTU

32	44	50.6	128	2	005400	005400 streptomycin
33	44	50.6	257	2	070307	070307 anopheles g
34	44	50.6	278	2	0720G9	0720G9 brachydanio
35	44	50.6	287	1	MF25_XENTLA	MF25_XENTLA
36	44	50.6	288	2	06GN48	06GN48 xenopus lae
37	44	50.6	568	2	084W52	084W52 xenopus lae
38	44	50.6	568	2	09LFB9	09LFB9 arabidopsis
39	44	50.6	949	2	09A9J5	09A9J5 caulobacter
40	44	50.6	1038	2	08PAY6	08PAY6 xanthomonas
41	43	49.4	99	2	06LHG2	06LHG2 photobacter
42	43	49.4	134	2	08MM82	08MM82 caenorhabdi
43	43	49.4	153	2	08GJ48	08GJ48 chlorobium
44	43	49.4	153	2	08GJ49	08GJ49 chlorobium
45	43	49.4	154	2	08GJ35	08GJ35 chlorobium

#### ALIGNMENTS

RESULT 1  
ID MYOD\_HUMAN STANDARD; PRT; 319 AA.  
AC PLS172;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Myoblast determination protein 1 (Myogenic factor 3) (Myf-3).  
GN Name=MYOD1; Synonyms=MYF3, MYOD;  
OS Homo sapiens (human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91212198; PubMed=1850513;  
RA Pearson-White S.H.;  
RL "Human Myod: cDNA and deduced amino acid sequence."  
RN Nucleic Acids Res. 19:1148-1148(1991).  
RN [2]  
RP SEQUENCE OF 53-319 FROM N.A.  
RC TISSUE=skelatal muscle;  
RX MEDLINE=90059960; PubMed=2583111;  
RA Braun T., Bober S., Buschhausen-Denker G., Kotz S., Grzeschik K.-H.,  
RA Arnold H.H.;  
RL "Differential expression of myogenic determination genes in muscle  
cells: possible autoactivation by the Myf gene products."  
EMBO J. 8:3617-3625(1989).  
RN [3]  
RP REVIEW ABOUT ACETYLATION AND DEACETYLATION.  
RX MEDLINE=21423399; PubMed=11532390; DOI=10.1016/S0959-437X(00)00224-0;  
RA McKinsey T.A., Zhang C.L., Olson E.N.;  
RL "Control of muscle development by dueling HMTs and HDACs."  
Curr. Opin. Genet. Dev. 11:497-504(2001).  
CC -1- FUNCTION: Involved in muscle differentiation (myogenic factor).  
Induces fibroblasts to differentiate into myoblasts. Activates  
muscle-specific promoters. Interacts with and is inhibited by the  
twist protein. This interaction probably involves the basic  
domain of both proteins (By similarity).  
CC -1- SUBUNIT: Efficient DNA binding requires dimerization with another  
bHLH protein. Seems to form active heterodimers with ITP-2.  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- PTM: Acetylated by a complex containing Epi300 and PCAF. The  
acetylation is essential to activate target genes. Conversely, its  
deacetylation by SIRT1 inhibits its function (By similarity).  
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
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CC -----  
 DR EMBL, X56677, CAA40000.1; -  
 DR EMBL, X17650, CAA35640.1; -  
 DR PIR, S26827, S26827.  
 DR HSP, P10085, IMDY.  
 DR TRANSFAC, T00519; -  
 DR TRANSFAC, T00525; -  
 DR Genew, HGNC:7611, MYO1.  
 DR MIM, 159370; -  
 DR GO, GO:0005634, C:nucleus, TAG.  
 DR GO, GO:0003705, F:RNA polymerase II transcription factor act... TAG.  
 DR GO, GO:0003713, F:transcription coactivator activity, TAG.  
 DR GO, GO:0007519, P:myogenesis, TAG.  
 DR GO, GO:0006468, P:protein amino acid phosphorylation, TAG.  
 DR GO, GO:0006357, P:regulation of transcription from Pol II promoter, TAG.  
 DR InterPro, IPR002546, Basic.  
 DR InterPro, IPR001092, HLH\_basic.  
 DR Pfam, PF00010, HLH, 1.  
 DR Pfam, PF01586, Basic, 1.  
 DR PROSITE, PS50868, HLH, 1.  
 DR Acetylation, Developmental protein, Differentiation, DNA-binding;  
 KW Myogenesis; Nuclear protein; transcription regulation.  
 FT DNA\_BIND 109 121 Basic motif.  
 FT DOMAIN 122 161 Helix-loop-helix motif.  
 FT CONFLICT 124 124 K -> E (in Ref. 2).  
 SO SEQUENCE 319 AA, 34490 MW, AAE935C154318770 CRC64,

Query Match 100.0%; Score 87; DB 1; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YSGPFGARRRNCYE 15  
 DB 212 YSGPFGARRRNCYE 226